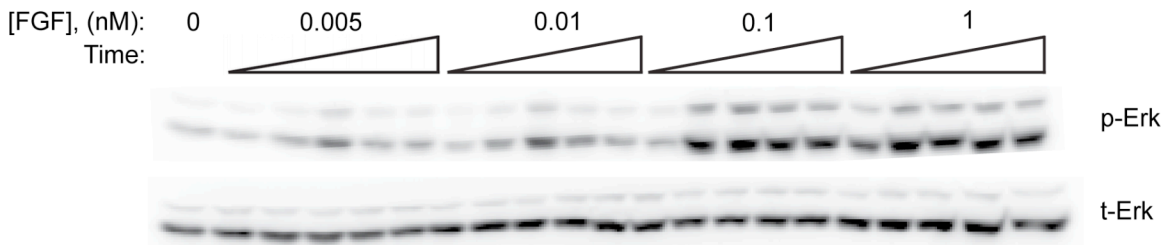

Figure S1. Characterization of FGF-stimulated ERK phosphorylation. NIH 3T3 fibroblasts were stimulated with FGF-2 at the indicated concentrations, and phosphorylation time courses of ERK1/2 (p-Erk) were measured by quantitative immunoblotting alongside total ERK (t-Erk) as a loading control. Stimulation times were 5, 15, 30, 60, and 120 minutes, and the blots shown are representative of six independent experiments. The results indicate that the response is saturated for FGF-2 concentrations of 0.1 nM and higher, whereas 0.01 nM FGF-2 is a subsaturating dose.

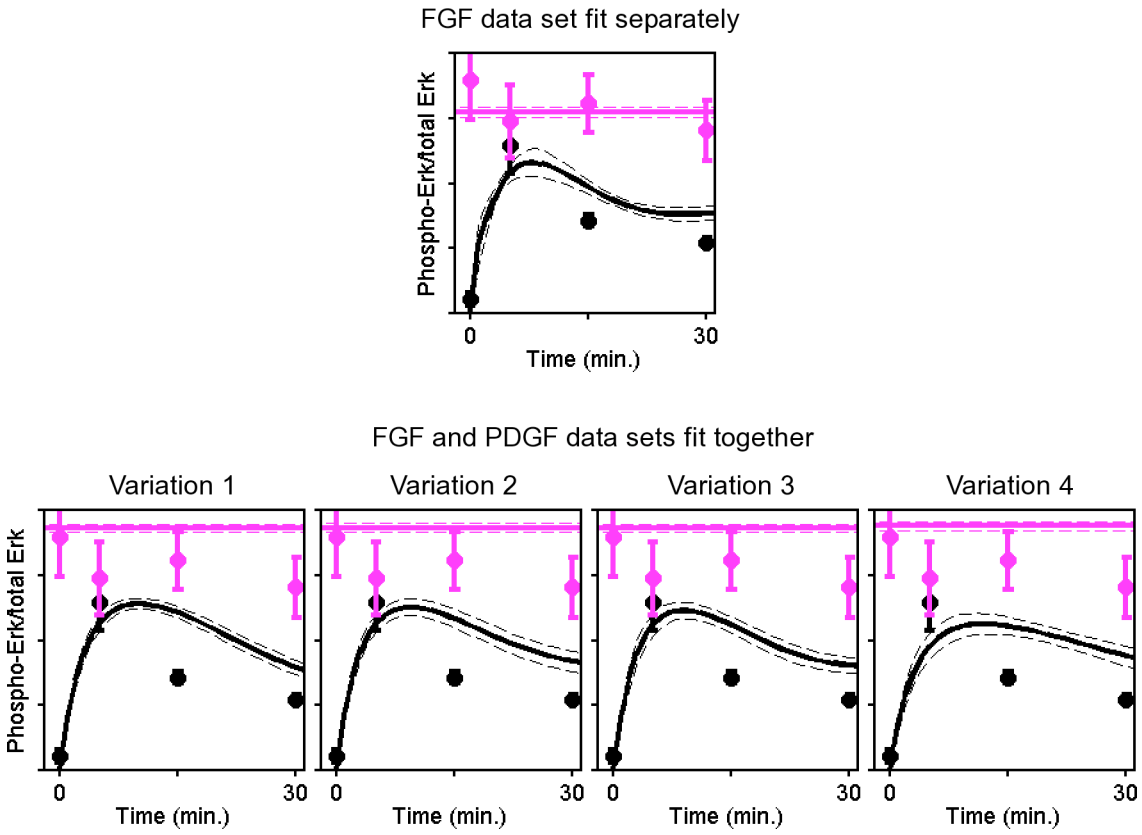

Figure S2. Additional ERK phosphorylation data used to constrain model-data alignment. These results accompany Figs. 3 and 5. In each plot here, the data are the same. NIH 3T3 cells were pretreated with either phorbol ester (200 nM PMA; magenta) or DMSO vehicle only (black) for 15 minutes, and FGF-2 was added to a final concentration of 1 nM at time zero. Time courses of ERK phosphorylation were measured by quantitative immunoblotting, with values normalized as previously described and reported as mean ± s.e.m. in arbitrary units (n = 3). Solid curves are ensemble means of the indicated model fits, and the dashed curves are mean ± s.d. (n = 10,000).

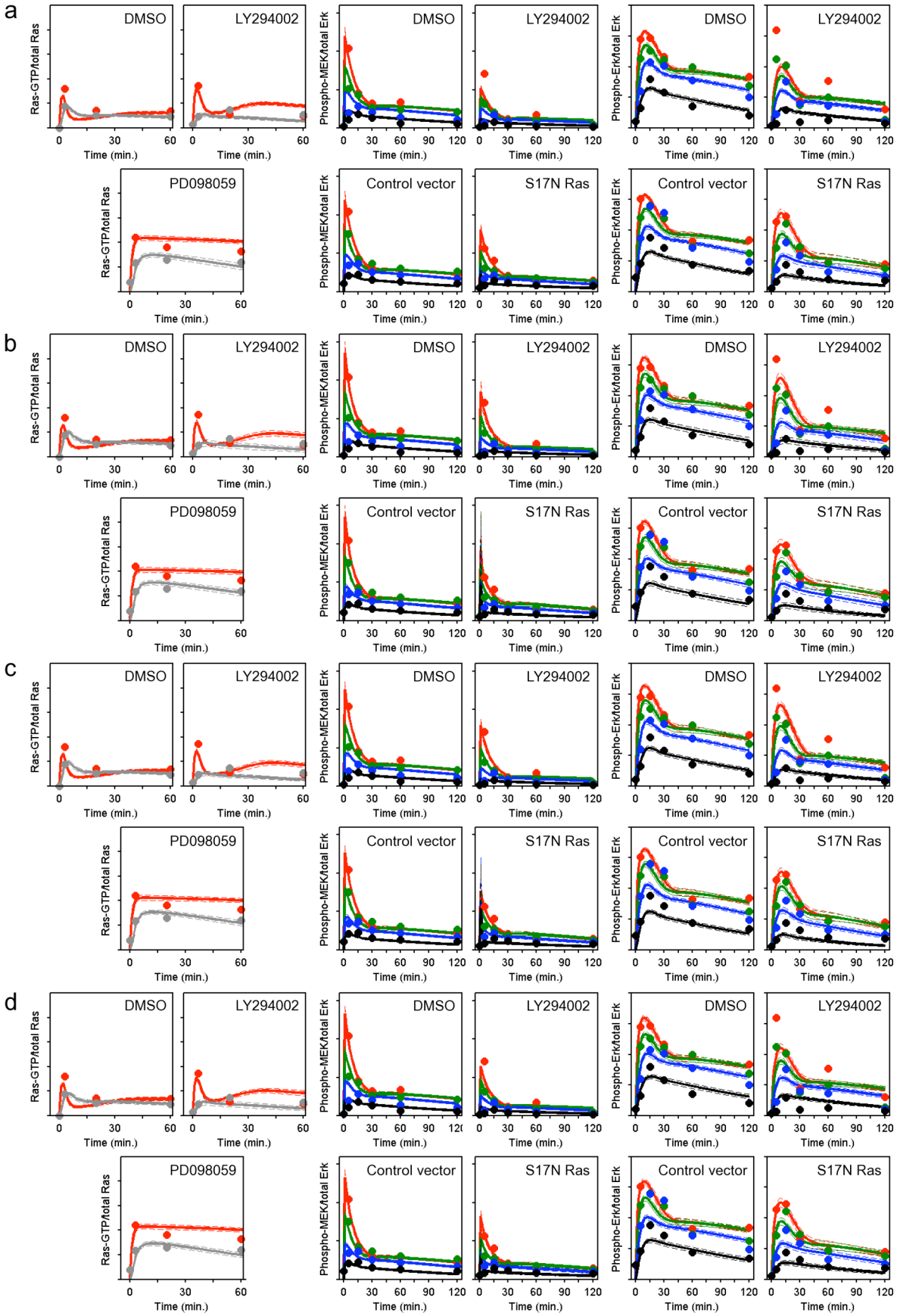
a
b
c
d
DMSO
LY294002
PD098059
Control vector
S17N Ras
Ras-GTP/total Ras
Phospho-MEK/total Erk
Phospho-Erk/total Erk
Time (min.)

Figure S3. Alignment of ensemble-averaged models fit to both FGF and PDGF receptor signalling networks: quality of fit to archival PDGF data. These results accompany Fig. 5. Each row, *a–d*, shows the relative quality of fit to previously published PDGF data, corresponding respectively to Fig. 5 *a–d*. The PDGF-BB concentration used for each time course are colour-coded as follows. Red: 1 nM; green: 300 pM; blue: 100 pM; gray: 50 pM; black: 30 pM.